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PCT/DK99/00481

1

SEQUENCE LISTING

<110> M&E Biotech A/S
HALKIER, Torben
HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand
Activity

<130> 22021 PC 1

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<141>

<160> 35

<170> PatentIn Ver. 2.1

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<211> 2271

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (185)..(1138)

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cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180
cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tgc 229
Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
1 5 10 15
gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
20 25 30
gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325
Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
35 40 45
atg ttc gtg gcc ctg ctg ggg ctg ggg ctg gcc cag gtt gtc tgc agc 373
Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60

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for
910

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 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
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tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469
 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
 80 85 90 95

aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517
 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
 100 105 110

ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565
 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
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 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu
 130 135 140

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 Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys
 145 150 155

ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc 709
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 160 165 170 175

cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cg 757
 Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
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 195 200 205

gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga 853
 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
 210 215 220

cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg 901
 His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
 225 230 235

gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg 949
 Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
 240 245 250 255

atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat 997
 Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
 260 265 270

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 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
 275 280 285

gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
 290 295 300

gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga 1138
 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 305 310 315

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<212> PRT

<213> Homo sapiens

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 35 40 45

Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 50 55 60

Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 65 70 75 80

Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 85 90 95

Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 100 105 110

Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 115 120 125

Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 130 135 140

Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 145 150 155 160

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 165 170 175

Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 180 185 190

Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 195 200 205

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 210 215 220

His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 225 230 235 240

Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 245 250 255

Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe

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260	265	270
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Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp		
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 <223> Transmembrane domain

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 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
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 gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc 144
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc 192
 Met Phe Leu Ala Leu Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata 240
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80

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tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa	288
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu	
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aac gca ggt ttg cag gac tgc act ctg gag agt gaa gac aca cta cct	336
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro	
100 105 110	
gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag	384
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys	
115 120 125	
gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct	432
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala	
130 135 140	
atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag	480
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu	
145 150 155 160	
gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tgc	528
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser	
165 170 175	
ggc tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg	576
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp	
180 185 190	
gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac	624
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn	
195 200 205	
caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat	672
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His	
210 215 220	
gaa aca tgc gga agc gta cct aca gac tat ctt cag ctg atg gtg tat	720
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr	
225 230 235 240	
gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa	768
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys	
245 250 255	
gga ggg agc acg aaa aac tgg tgc ggc aat tct gaa ttc cac ttt tat	816
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr	
260 265 270	
tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att	864
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile	
275 280 285	

agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg 912
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205

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Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
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gggagagaac gatcgcgagg cagggcgccc gaactccggg cgccgcgcc atg cgc cgg 178

Met Arg Arg

1

gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc 226

Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly

5

10

15

agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct 274

Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser

20

25

30

35

gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg 322

Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu

40

45

50

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55 60 65	
ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata tca gaa gac	418
Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp	
70 75 80	
agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt	466
Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly	
85 90 95	
ttg cag gac tgc act ctg gag agt gaa gac aca cta cct gac tcc tgc	514
Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys	
100 105 110 115	
agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa	562
Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln	
120 125 130	
cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa	610
His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu	
135 140 145	
ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag gcc cag cca	658
Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro	
150 155 160	
ttt gca cac ctc acc atc aat gct gcc agc atc cca tgc ggt tcc cat	706
Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His	
165 170 175	
aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc	754
Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile	
180 185 190 195	
tct aac atg acg tta agc aac gga aaa cta agg gtt aac caa gat ggc	802
Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly	
200 205 210	
ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat gaa aca tgc	850
Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser	
215 220 225	
gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa	898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys	
230 235 240	
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggc agc	946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser	
245 250 255	

acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat 994
 Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn
 260 265 270 275

 gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att agc att cag 1042
 Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln
 280 285 290

 gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg acg tac ttt 1090
 Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe
 295 300 305

 ggg gct ttc aaa gtt cag gac ata gac tga gactcatttc gtggaacatt 1140
 Gly Ala Phe Lys Val Gln Asp Ile Asp
 310 315

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 taagactact aagagacatg gccacagggtg tatgaaactc acagccctct ctcttgagcc 1260
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<212> PRT

<213> Mus musculus

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 35 40 45

Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60

Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80

Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95

Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110

Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125

Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140

Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160

Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175

Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190

Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205

Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220

Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240

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12

Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255

Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
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Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
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<223> Description of Artificial Sequence: Synthetic PCR
 product with optimum codons for E. coli and P.
 pastoris expression

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<222> (43)..(84)

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<223> C-terminal part of *Saccharomyces cerevisiae*
 alpha-mating factor

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<223> Encoding wild type murine OPGL, residues 158-316

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13

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 His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
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cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt 144
 Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
 35 40 45

tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct 192
 Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
 50 55 60

aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt aac cag 240
 Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
 65 70 75 80

gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa 288
 Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
 85 90 95

acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt 336
 Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
 100 105 110

gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt 384
 Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
 115 120 125

ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct 432
 Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
 130 135 140

atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct 480
 Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
 145 150 155 160

atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc 528
 Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
 165 170 175

tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag 564
 Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 180 185

<210> 8

<211> 187

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic PCR
 product with optimum codons for E. coli and P.
 pastoris expression

0978726
 034404

14

<400> 8

Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
 1 5 10 15

His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
 20 25 30

Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
 35 40 45

Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
 50 55 60

Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
 65 70 75 80

Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
 85 90 95

Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
 100 105 110

Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
 115 120 125

Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
 130 135 140

Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
 145 150 155 160

Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
 165 170 175

Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 180 185

<210> 9

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA encoding
 murine OPGL, residues 158-316, fused to His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

09787125 031401

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(519)

<223> Murine OPGL, residues 158-316

<400> 9

atg	aaa	cac	caa	cac	caa	cat	caa	cat	caa	cat	caa	aaa	cct	48
Met	Lys	His	Gln	His	Gln	His	Gln	His	Gln	His	Gln	Lys	Pro	
1				5				10				15		

gaa	gct	cag	cca	ttc	gct	cat	ctg	acc	atc	aac	gct	gca	tcg	atc	cct	96
Glu	Ala	Gln	Pro	Phe	Ala	His	Leu	Thr	Ile	Asn	Ala	Ala	Ser	Ile	Pro	
			20					25					30			

tct	ggt	tct	cat	aaa	gtt	acc	ctg	tct	tct	tgg	tat	cac	gac	cgc	ggt	144
Ser	Gly	Ser	His	Lys	Val	Thr	Leu	Ser	Ser	Trp	Tyr	His	Asp	Arg	Gly	
			35				40					45				

tgg	gct	aaa	atc	tct	aac	atg	acc	ctg	tct	aac	ggt	aaa	ctg	aga	gtt	192
Trp	Ala	Lys	Ile	Ser	Asn	Met	Thr	Leu	Ser	Asn	Gly	Lys	Leu	Arg	Val	
		50				55					60					

aac	cag	gac	ggt	ttc	tac	tac	ctg	tac	gct	aac	atc	tgt	ttc	aga	cat	240
Asn	Gln	Asp	Gly	Phe	Tyr	Leu	Tyr	Ala	Asn	Ile	Cys	Phe	Arg	His		
65				70					75				80			

cac	gaa	acc	tct	ggt	tct	gtt	cca	acc	gac	tac	ctg	cag	ctg	atg	gtt	288
His	Glu	Thr	Ser	Gly	Ser	Val	Pro	Thr	Asp	Tyr	Leu	Gln	Leu	Met	Val	
				85					90					95		

tac	gtt	gtt	aaa	acc	tct	atc	aaa	atc	cca	tct	tca	cat	aac	ctg	atg	336
Tyr	Val	Val	Lys	Thr	Ser	Ile	Lys	Ile	Pro	Ser	Ser	His	Asn	Leu	Met	
			100					105						110		

aaa	ggt	ggt	tct	acc	aaa	aac	tgg	tct	ggt	aac	tct	gaa	ttc	cat	ttc	384
Lys	Gly	Gly	Ser	Thr	Lys	Asn	Trp	Ser	Gly	Asn	Ser	Glu	Phe	His	Phe	
		115					120					125				

tac	tct	atc	aac	gtt	ggt	ggt	ttc	ttc	aaa	ctg	aga	gct	ggt	gaa	gaa	432
Tyr	Ser	Ile	Asn	Val	Gly	Gly	Phe	Phe	Lys	Leu	Arg	Ala	Gly	Glu	Glu	
		130				135					140					

atc	tct	atc	cag	gtt	tct	aac	cct	tct	ctg	ctg	gac	cca	gac	cag	gac	480
Ile	Ser	Ile	Gln	Val	Ser	Asn	Pro	Ser	Leu	Leu	Asp	Pro	Asp	Gln	Asp	
145					150					155				160		

gct	acc	tac	ttc	ggg	gcc	ttc	aaa	gtt	cag	gac	atc	gac				519
Ala	Thr	Tyr	Phe	Gly	Ala	Phe	Lys	Val	Gln	Asp	Ile	Asp				
				165					170							

09787426.031401

<210> 10
 <211> 173
 <212> PRT
 <213> Artificial Sequence
 <223> Description of Artificial Sequence: DNA encoding
 murine OPGL, residues 158-316, fused to His tag

<400> 10
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
 115 120 125
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
 130 135 140
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 145 150 155 160
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 165 170

<210> 11
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 with C to S
 mutation, and His tag

09787126.034401

<220>
 <221> CDS
 <222> (1)..(519)

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(228)
 <223> Murine OPGL, residues 158-219

<220>
 <221> misc_feature
 <222> (232)..(519)
 <223> Murine OPGL, residues 221-316

<220>
 <221> mutation
 <222> (229)..(231)
 <223> tgt (Cys) to tcc (Ser)

<220>

<400> 11
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15
 gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30
 tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45
 tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60
 aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat 240
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
 65 70 75 80
 cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

18

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384
 Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
 115 120 125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aqa gct ggt gaa gaa 432
 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
 130 135 140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480
 Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 145 150 155 160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519
 Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 165 170

<210> 12

<211> 173

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 with C to S
 mutation, and His tag

<400> 12

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
 115 120 125

09787125-034401

19

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
 130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 165 170

<210> 13

<211> 564

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 modified by
 introduction of tetanus toxoid P30 epitope, and
 His tag

<220>

<221> CDS

<222> (1)..(564)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(336)

<223> Murine OPGL, residues 158-255

<220>

<221> misc_feature

<222> (337)..(399)

<223> Tetanus toxoid P30 epitope

<220>

<221> misc_feature

<222> (400)..(564)

<223> Murine OPGL, residues 262-316

<400> 13

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro

1

5

10

15

09787126-031401

20

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336
 Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110

ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct 384
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 115 120 125

gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac 432
 Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 130 135 140

tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc 480
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 145 150 155 160

tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct 528
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 165 170 175

acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 564
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 180 185

<210> 14

<211> 188

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion of
 murine OPGL, residues 158-316 modified by
 introduction of tetanus toxoid P30 epitope, and
 His tag

09787126-031401

<400> 14

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
 100 105 110

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 115 120 125

Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 130 135 140

Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 145 150 155 160

Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 165 170 175

Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
 180 185

<210> 15

<211> 546

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 between murine OPGL, residues 158-316 with tetanus
 toxoid P2 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(546)

09787126 031401

<220>
 <221> misc_binding
 <222> (1)..(42)
 <223> His tag

<220>
 <221> misc_feature
 <222> (43)..(336)
 <223> Murine OPGL, residues 158-255

<220>
 <221> misc_feature
 <222> (382)..(546)
 <223> Murine OPGL, residues 262-316

<220>
 <221> misc_feature
 <222> (337)..(381)
 <223> Tetanus toxoid P2 epitope

<400> 15
 atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
 Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
 Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
 His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336
 Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
 100 105 110

cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
 115 120 125

09787126.031401

23

tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt 432
 Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 130 135 140

ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac 480
 Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 145 150 155 160

cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc 528
 Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 165 170 175

aaa gtt cag gac atc gac 546
 Lys Val Gln Asp Ile Asp
 180

<210> 16

<211> 182

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion
 between murine OPGL, residues 158-316 with tetanus
 toxoid P2 epitope introduced, and His tag

<400> 16

Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
 35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
 50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
 85 90 95

Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
 100 105 110

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
 115 120 125

Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
 130 135 140

09787126.031401

24

Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
 145 150 155 160

Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
 165 170 175

Lys Val Gln Asp Ile Asp
 180

<210> 17

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion between
 murine OPGL, residues 158-316 with tetanus toxoid
 P2 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(432)

<223> Murine OPGL, residues 158-287

<220>

<221> misc_feature

<222> (478)..(519)

<223> Murine OPGL, residues 303-316

<220>

<221> misc_feature

<222> (433)..(477)

<223> Tetanus toxoid P2 epitope

<400> 17

atg aaa cac caa cac caa cat caa cat caa cat caa aaa cct 48
 Met Lys His Gln His Gln His Gln His Gln His Gln Lys Pro
 1 5 10 15

gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
 20 25 30

09787126 031401

26

35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65 70 75 80

His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
85 90 95

Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
130 135 140

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 19

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P30 epitope introduced, and His tag

<220>

<221> CDS

<222> (1)..(519)

<220>

<221> misc_binding

<222> (1)..(42)

<223> His tag

<220>

<221> misc_feature

<222> (43)..(231)

<223> Murine OPGL, residues 158-220

<220>

09787125.031401
 1041E0" 921/28/60

del
 910
 Cont

<221> misc_feature

<222> (295)..(519)

<223> Murine OPGL, residues 242-316

<220>

<221> misc_feature

<222> (232)..(294)

<223> Tetanus toxoid P30 epitope

<400> 19

atg aaa cat caa cac caa cat caa cat caa cat caa cat caa aaa cct 48

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro

1

5

10

15

gaa gct cag caa ttc gct cat ctg acc atc aac gct gca tcg atc cct 96

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro

20

25

30

tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly

35

40

45

tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val

50

55

60

aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac 240

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn

65

70

75

80

ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac 288

Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His

85

90

95

ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg 336

Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met

100

105

110

aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc 384

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe

115

120

125

tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa 432

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu

130

135

140

atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac 480

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp

145

150

155

160

gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac 519

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp

165

170

09737125.031401

Sub
A10
cont

<210> 20

<211> 173

<212> PPT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P30 epitope introduced, and His tag

<400> 20

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15

Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
20 25 30

Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
35 40 45

Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60

Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
65 70 75 80

Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
85 90 95

Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110

Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
115 120 125

Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
130 135 140

Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145 150 155 160

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 21

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR
primer

FILED "SET 28/60"

Sub
a10
Cont

<400> 21
agctgcagggt agtcggttgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60
gcgtacag 68

<210> 22
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 22
ctcatctgac catcaacgct gcat 24

<210> 23
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 23
tttcggtacc ctccagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60
gtag 64

<210> 24
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 24
tgagggtacc gaaagtttct gcttctcacc tggaagttaa aaccctatc aaaatccaat 60
c 61

<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR

09787436 031401

Sub
a/o
cont

primer

<400> 25
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aacatcaggt tatgtgaaga 60
ttg 63

<210> 26
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 26
tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60
at 62

<210> 27
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 27
tacctgcagc tgatggttta cgttgttaaa acccctatca aaatccaatc ttcacataac 60
ctgatgcagt acatcaaag 79

<210> 28
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR
primer

<400> 28
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60
ttgatgtact gcatcagggt atg 83

<210> 29
<211> 49
<212> DNA
<213> Artificial Sequence

09787126.031401

Sub
A10
Cont

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 29

gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg

49

<210> 30

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 30

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53

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 31

cttactagtc gatgtcctga actttg

26

<210> 32

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 32

agtggaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60
aagatgggat ttg 74

<210> 33

<211> 65

<212> DNA

<213> Clostridium tetani

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Sul
a10
cont

<210> 34
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 34
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

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<210> 35
<211> 21
<212> PRT
<213> Clostridium tetani
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<400> 35
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15

Ala Ser His Leu Glu
20

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